

SEQUENCE LISTING

(1) GENERAL INFORMATION:

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(i) APPLICANTS: Wallner, Barbara P.
Cooper, Kevin D.

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(ii) TITLE OF INVENTION: Method of Prophylaxis or Treatment of Antigen
Presenting Cell Driven Skin Conditions Using
Inhibitors of the CD2/LFA-3 Interaction

(iii) NUMBER OF SEQUENCES: 8

15

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: LAHIVE & COCKFIELD
(B) STREET: 60 State Street, Suite 510
(C) CITY: Boston
(D) STATE: Massachusetts
(E) COUNTRY: USA
(F) ZIP: 02109-1875

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

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(vi) CURRENT APPLICATION DATA:

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(A) APPLICATION NUMBER:
(B) FILING DATE:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/US92/08755
(B) FILING DATE: 06-OCT-1992

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(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/862,022
(B) FILING DATE: 12-APR-1992

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(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/770,969
(B) FILING DATE: 07-OCT-1991

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(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Myers, Louis (PLM)
(B) REGISTRATION NUMBER: 35,965
(C) REFERENCE/DOCKET NUMBER: BGP-111CP

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(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617) 227-7400
(B) TELEFAX: (617) 227-5941

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 753 base pairs
(B) TYPE: nucleic acid

030301 3006260

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..750

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(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 1..84

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(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 85..750

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(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1..750
(D) OTHER INFORMATION: /note= "Human transmembrane LFA-3"

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(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 646
(D) OTHER INFORMATION: /note= "Transmembrane domain"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG GTT GCT GGG AGC GAC GCG GGG CGG GCC CTG GGG GTC CTC AGC GTG 48
Met Val Ala Gly Ser Asp Ala Gly Arg Ala Leu Gly Val Leu Ser Val
-28 -25 -20 -15

35

GTC TGC CTG CTG CAC TGC TTT GGT TTC ATC AGC TGT TTT TCC CAA CAA 96
Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe Ser Gln Gln
-10 -5 1

40

ATA TAT GGT GTT GTG TAT GGG AAT GTA ACT TTC CAT GTA CCA AGC AAT 144
Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn
5 10 15 20

45

GTG CCT TTA AAA GAG GTC CTA TGG AAA AAA CAA AAG GAT AAA GTT GCA 192
Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala
25 30 35

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GAA CTG GAA AAT TCT GAA TTC AGA GCT TTC TCA TCT TTT AAA AAT AGG 240
Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg
40 45 50

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GTT TAT TTA GAC ACT GTG TCA GGT AGC CTC ACT ATC TAC AAC TTA ACA 288
Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr
55 60 65

TCA TCA GAT GAA GAT GAG TAT GAA ATG GAA TCG CCA AAT ATT ACT GAT 336
Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp
70 75 80

00502T 3406260

ACC ATG AAG TTC TTT CTT TAT GTG CTT GAG TCT CTT CCA TCT CCC ACA 384
 Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro Ser Pro Thr
 85 90 95 100

5 CTA ACT TGT GCA TTG ACT AAT GGA AGC ATT GAA GTC CAA TGC ATG ATA 432
 Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln Cys Met Ile
 105 110 115

10 CCA GAG CAT TAC AAC AGC CAT CGA GGA CTT ATA ATG TAC TCA TGG GAT 480
 Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr Ser Trp Asp
 120 125 130

15 TGT CCT ATG GAG CAA TGT AAA CGT AAC TCA ACC AGT ATA TAT TTT AAG 528
 Cys Pro Met Glu Gln Cys Lys Arg Asn Ser Thr Ser Ile Tyr Phe Lys
 135 140 145

20 ATG GAA AAT GAT CTT CCA CAA AAA ATA CAG TGT ACT CTT AGC AAT CCA 576
 Met Glu Asn Asp Leu Pro Gln Lys Ile Gln Cys Thr Leu Ser Asn Pro
 150 155 160

TTA TTT AAT ACA ACA TCA TCA ATC ATT TTG ACA ACC TGT ATC CCA AGC 624
 Leu Phe Asn Thr Thr Ser Ser Ile Ile Leu Thr Thr Cys Ile Pro Ser
 165 170 175 180

25 AGC GGT CAT TCA AGA CAC AGA TAT GCA CTT ATA CCC ATA CCA TTA GCA 672
 Ser Gly His Ser Arg His Arg Tyr Ala Leu Ile Pro Ile Pro Leu Ala
 185 190 195

30 GTA ATT ACA ACA TGT ATT GTG CTG TAT ATG AAT GGT ATT CTG AAA TGT 720
 Val Ile Thr Thr Cys Ile Val Leu Tyr Met Asn Gly Ile Leu Lys Cys
 200 205 210

35 GAC AGA AAA CCA GAC AGA ACC AAC TCC AAT TGA 753
 Asp Arg Lys Pro Asp Arg Thr Asn Ser Asn
 215 220

(2) INFORMATION FOR SEQ ID NO:2:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 250 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- 45 (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

50 Met Val Ala Gly Ser Asp Ala Gly Arg Ala Leu Gly Val Leu Ser Val
 -28 -25 -20 -15

Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe Ser Gln Gln
 -10 -5 1

55 Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn
 5 10 15 20

Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala
 25 30 35

Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg
 40 45 50
 5 Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr
 55 60 65
 Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp
 70 75 80
 10 Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro Ser Pro Thr
 85 90 95 100
 Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln Cys Met Ile
 15 105 110 115
 Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr Ser Trp Asp
 120 125 130
 20 Cys Pro Met Glu Gln Cys Lys Arg Asn Ser Thr Ser Ile Tyr Phe Lys
 135 140 145
 Met Glu Asn Asp Leu Pro Gln Lys Ile Gln Cys Thr Leu Ser Asn Pro
 150 155 160
 25 Leu Phe Asn Thr Thr Ser Ile Ile Leu Thr Thr Cys Ile Pro Ser
 165 170 175 180
 Ser Gly His Ser Arg His Arg Tyr Ala Leu Ile Pro Ile Pro Leu Ala
 30 185 190 195
 Val Ile Thr Thr Cys Ile Val Leu Tyr Met Asn Gly Ile Leu Lys Cys
 200 205 210
 35 Asp Arg Lys Pro Asp Arg Thr Asn Ser Asn
 215 220

(2) INFORMATION FOR SEQ ID NO:3:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 723 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 45 (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
- 50 (A) NAME/KEY: CDS
 (B) LOCATION: 1..720
- (ix) FEATURE:
- 55 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 1..84
- (ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 85..720

005027 5344260

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..720

5 (D) OTHER INFORMATION: /note= "Human PI-linked LFA-3"

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 568..720

10 (D) OTHER INFORMATION: /note= "Signal sequence for
PI-linkage"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

15 ATG GTT GCT GGG AGC GAC GCG GGG CGG GCC CTG GGG GTC CTC AGC GTG 48
Met Val Ala Gly Ser Asp Ala Gly Arg Ala Leu Gly Val Leu Ser Val
-28 -25 -20 -15

20 GTC TGC CTG CTG CAC TGC TTT GGT TTC ATC AGC TGT TTT TCC CAA CAA 96
Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe Ser Gln Gln
-10 -5 1

25 ATA TAT GGT GTT GTG TAT GGG AAT GTA ACT TTC CAT GTA CCA AGC AAT 144
Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn
5 10 15 20

30 GTG CCT TTA AAA GAG GTC CTA TGG AAA AAA CAA AAG GAT AAA GTT GCA 192
Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala
25 30 35

35 GAA CTG GAA AAT TCT GAA TTC AGA GCT TTC TCA TCT TTT AAA AAT AGG 240
Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg
40 45 50

40 GTT TAT TTA GAC ACT GTG TCA GGT AGC CTC ACT ATC TAC AAC TTA ACA 288
Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr
55 60 65

45 TCA TCA GAT GAA GAT GAG TAT GAA ATG GAA TCG CCA AAT ATT ACT GAT 336
Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp
70 75 80

50 ACC ATG AAG TTC TTT CTT TAT GTG CTT GAG TCT CTT CCA TCT CCC ACA 384
Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro Ser Pro Thr
85 90 95 100

55 CTA ACT TGT GCA TTG ACT AAT GGA AGC ATT GAA GTC CAA TGC ATG ATA 432
Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln Cys Met Ile
105 110 115

CCA GAG CAT TAC AAC AGC CAT CGA GGA CTT ATA ATG TAC TCA TGG GAT 480
Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr Ser Trp Asp
120 125 130

TGT CCT ATG GAG CAA TGT AAA CGT AAC TCA ACC AGT ATA TAT TTT AAG 528
Cys Pro Met Glu Gln Cys Lys Arg Asn Ser Thr Ser Ile Tyr Phe Lys
135 140 145

003046260

ATG GAA AAT GAT CTT CCA CAA AAA ATA CAG TGT ACT CTT AGC AAT CCA 576
 Met Glu Asn Asp Leu Pro Gln Lys Ile Gln Cys Thr Leu Ser Asn Pro
 150 155 160
 5 TTA TTT AAT ACA ACA TCA TCA ATC ATT TTG ACA ACC TGT ATC CCA AGC 624
 Leu Phe Asn Thr Thr Ser Ser Ile Ile Leu Thr Thr Cys Ile Pro Ser
 165 170 175 180
 AGC GGT CAT TCA AGA CAC AGA TAT GCA CTT ATA CCC ATA CCA TTA GCA 672
 10 Ser Gly His Ser Arg His Arg Tyr Ala Leu Ile Pro Ile Pro Leu Ala
 185 190 195
 GTA ATT ACA ACA TGT ATT GTG CTG TAT ATG AAT GGT ATG TAT GCT TTT 720
 15 Val Ile Thr Thr Cys Ile Val Leu Tyr Met Asn Gly Met Tyr Ala Phe
 200 205 210
 TAA 723

20 (2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 240 amino acids

(B) TYPE: amino acid

25 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

30 Met Val Ala Gly Ser Asp Ala Gly Arg Ala Leu Gly Val Leu Ser Val
 -28 -25 -20 -15
 35 Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe Ser Gln Gln
 -10 -5 1
 Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn
 5 10 15 20
 40 Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala
 25 30 35
 Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg
 40 45 50
 45 Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr
 55 60 65
 50 Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp
 70 75 80
 Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro Ser Pro Thr
 85 90 95 100
 55 Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln Cys Met Ile
 105 110 115
 Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr Ser Trp Asp
 120 125 130

CC361-3436263

Cys Pro Met Glu Gln Cys Lys Arg Asn Ser Thr Ser Ile Tyr Phe Lys
 135 140 145
 5 Met Glu Asn Asp Leu Pro Gln Lys Ile Gln Cys Thr Leu Ser Asn Pro
 150 155 160
 Leu Phe Asn Thr Thr Ser Ser Ile Ile Leu Thr Thr Cys Ile Pro Ser
 165 170 175 180
 10 Ser Gly His Ser Arg His Arg Tyr Ala Leu Ile Pro Ile Pro Leu Ala
 185 190 195
 Val Ile Thr Thr Cys Ile Val Leu Tyr Met Asn Gly Met Tyr Ala Phe
 15 200 205 210

(2) INFORMATION FOR SEQ ID NO:5:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1056 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 25 (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 30 (A) NAME/KEY: CDS
 (B) LOCATION: 1..1053
- (ix) FEATURE:
 35 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 1..72
- (ix) FEATURE:
 40 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 73..1053
- (ix) FEATURE:
 45 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..1053
 (D) OTHER INFORMATION: /note= "Human CD2"
- (ix) FEATURE:
 50 (A) NAME/KEY: misc_feature
 (B) LOCATION: 628..702
 (D) OTHER INFORMATION: /note= "Transmembrane domain"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

55 ATG AGC TTT CCA TGT AAA TTT GTA GCC AGC TTC CTT CTG ATT TTC AAT 48
 Met Ser Phe Pro Cys Lys Phe Val Ala Ser Phe Leu Leu Ile Phe Asn
 -24 -20 -15 -10
 GTT TCT TCC AAA GGT GCA GTC TCC AAA GAG ATT ACG AAT GCC TTG GAA 96
 Val Ser Ser Lys Gly Ala Val Ser Lys Glu Ile Thr Asn Ala Leu Glu

	ACC	TGG	GGT	CCC	TTG	GGT	CAG	GAC	ATC	AAC	TTG	GAC	ATT	CCT	AGT	TTT	144
5	Thr	Trp	Gly	Ala	Leu	Gly	Gln	Asp	Ile	Asn	Leu	Asp	Ile	Pro	Ser	Phe	
	10						15					20					
	CAA	ATG	AGT	GAT	GAT	ATT	GAC	GAT	ATA	AAA	TGG	GAA	AAA	ACT	TCA	GAC	192
	Gln	Met	Ser	Asp	Asp	Ile	Asp	Asp	Ile	Lys	Trp	Glu	Lys	Thr	Ser	Asp	
	25					30					35					40	
10	AAG	AAA	AAG	ATT	GCA	CAA	TTC	AGA	AAA	GAG	AAA	GAG	ACT	TTC	AAG	GAA	240
	Lys	Lys	Lys	Ile	Ala	Gln	Phe	Arg	Lys	Glu	Lys	Glu	Thr	Phe	Lys	Glu	
					45					50					55		
15	AAA	GAT	ACA	TAT	AAG	CTA	TTT	AAA	AAT	GGA	ACT	CTG	AAA	ATT	AAG	CAT	288
	Lys	Asp	Thr	Tyr	Lys	Leu	Phe	Lys	Asn	Gly	Thr	Leu	Lys	Ile	Lys	His	
					60				65					70			
	CTG	AAG	ACC	GAT	GAT	CAG	GAT	ATC	TAC	AAG	GTA	TCA	ATA	TAT	GAT	ACA	336
20	Leu	Lys	Thr	Asp	Asp	Gln	Asp	Ile	Tyr	Lys	Val	Ser	Ile	Tyr	Asp	Thr	
					75			80						85			
	AAA	GGA	AAA	AAT	GTG	TTG	GAA	AAA	ATA	TTT	GAT	TTG	AAG	ATT	CAA	GAG	384
25	Lys	Gly	Lys	Asn	Val	Leu	Glu	Lys	Ile	Phe	Asp	Leu	Lys	Ile	Gln	Glu	
		90					95					100					
	AGG	GTC	TCA	AAA	CCA	AAG	ATC	TCC	TGG	ACT	TGT	ATC	AAC	ACA	ACC	CTG	432
	Arg	Val	Ser	Lys	Pro	Lys	Ile	Ser	Trp	Thr	Cys	Ile	Asn	Thr	Thr	Leu	
	105					110					115					120	
30	ACC	TGT	GAG	GTA	ATG	AAT	GGA	ACT	GAC	CCC	GAA	TTA	AAC	CTG	TAT	CAA	480
	Thr	Cys	Glu	Val	Met	Asn	Gly	Thr	Asp	Pro	Glu	Leu	Asn	Leu	Tyr	Gln	
					125					130					135		
35	GAT	GGG	AAA	CAT	CTA	AAA	CTT	TCT	CAG	AGG	GTC	ATC	ACA	CAC	AAG	TGG	528
	Asp	Gly	Lys	His	Leu	Lys	Leu	Ser	Gln	Arg	Val	Ile	Thr	His	Lys	Trp	
					140				145					150			
	ACC	ACC	AGC	CTG	AGT	GCA	AAA	TTC	AAG	TGC	ACA	GCA	GGG	AAC	AAA	GTC	576
40	Thr	Thr	Ser	Leu	Ser	Ala	Lys	Phe	Lys	Cys	Thr	Ala	Gly	Asn	Lys	Val	
					155				160					165			
	AGC	AAG	GAA	TCC	AGT	GTC	GAG	CCT	GTC	AGC	TGT	CCA	GAG	AAA	GGT	CTG	624
45	Ser	Lys	Glu	Ser	Ser	Val	Glu	Pro	Val	Ser	Cys	Pro	Glu	Lys	Gly	Leu	
		170					175					180					
	GAC	ATC	TAT	CTC	ATC	ATT	GGC	ATA	TGT	GGA	GGA	GGC	AGC	CTC	TTG	ATG	672
	Asp	Ile	Tyr	Leu	Ile	Ile	Gly	Ile	Cys	Gly	Gly	Gly	Ser	Leu	Leu	Met	
	185					190					195					200	
50	GTC	TTT	GTG	GCA	CTG	CTC	GTT	TTC	TAT	ATC	ACC	AAA	AGG	AAA	AAA	CAG	720
	Val	Phe	Val	Ala	Leu	Leu	Val	Phe	Tyr	Ile	Thr	Lys</					

Ala Thr Glu Glu Arg Gly Arg Lys Pro His Gln Ile Pro Ala Ser Thr
 235 240 245

5 CCT CAG AAT CCA GCA ACT TCC CAA CAT CCT CCT CCA CCA CCT GGT CAT 864
 Pro Gln Asn Pro Ala Thr Ser Gln His Pro Pro Pro Pro Gly His
 250 255 260

10 CGT TCC CAG GCA CCT AGT CAT CGT CCC CCG CCT CCT GGA CAC CGT GTT 912
 Arg Ser Gln Ala Pro Ser His Arg Pro Pro Pro Pro Gly His Arg Val
 265 270 275 280

15 CAG CAC CAG CCT CAG AAG AGG CCT CCT GCT CCG TCG GGC ACA CAA GTT 960
 Gln His Gln Pro Gln Lys Arg Pro Pro Ala Pro Ser Gly Thr Gln Val
 285 290 295

CAC CAG CAG AAA GGC CCG CCC CTC CCC AGA CCT CGA GTT CAG CCA AAA 1008
 His Gln Gln Lys Gly Pro Pro Leu Pro Arg Pro Arg Val Gln Pro Lys
 300 305 310

20 CCT CCC CAT GGG GCA GCA GAA AAC TCA TTG TCC CCT TCC TCT AAT 1053
 Pro Pro His Gly Ala Ala Glu Asn Ser Leu Ser Pro Ser Ser Asn
 315 320 325

25 TAA 1056

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 351 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ser Phe Pro Cys Lys Phe Val Ala Ser Phe Leu Leu Ile Phe Asn
 -24 -20 -15 -10

40 Val Ser Ser Lys Gly Ala Val Ser Lys Glu Ile Thr Asn Ala Leu Glu
 -5 1 5

Thr Trp Gly Ala Leu Gly Gln Asp Ile Asn Leu Asp Ile Pro Ser Phe
 45 10 15 20

Gln Met Ser Asp Asp Ile Asp Asp Ile Lys Trp Glu Lys Thr Ser Asp
 25 30 35 40

50 Lys Lys Lys Ile Ala Gln Phe Arg Lys Glu Lys Glu Thr Phe Lys Glu
 45 50 55

Lys Asp Thr Tyr Lys Leu Phe Lys Asn Gly Thr Leu Lys Ile Lys His
 60 65 70

55 Leu Lys Thr Asp Asp Gln Asp Ile Tyr Lys Val Ser Ile Tyr Asp Thr
 75 80 85

Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Asp Leu Lys Ile Gln Glu

003027 3406263

	90	95	100
	Arg Val Ser Lys Pro Lys Ile Ser Trp Thr Cys Ile Asn Thr Thr Leu		
	105	110	115 120
5	Thr Cys Glu Val Met Asn Gly Thr Asp Pro Glu Leu Asn Leu Tyr Gln		
	125	130	135
	Asp Gly Lys His Leu Lys Leu Ser Gln Arg Val Ile Thr His Lys Trp		
10	140	145	150
	Thr Thr Ser Leu Ser Ala Lys Phe Lys Cys Thr Ala Gly Asn Lys Val		
	155	160	165
	Ser Lys Glu Ser Ser Val Glu Pro Val Ser Cys Pro Glu Lys Gly Leu		
15	170	175	180
	Asp Ile Tyr Leu Ile Ile Gly Ile Cys Gly Gly Gly Ser Leu Leu Met		
20	185	190	195 200
	Val Phe Val Ala Leu Leu Val Phe Tyr Ile Thr Lys Arg Lys Lys Gln		
	205	210	215
	Arg Ser Arg Arg Asn Asp Glu Glu Leu Glu Thr Arg Ala His Arg Val		
25	220	225	230
	Ala Thr Glu Glu Arg Gly Arg Lys Pro His Gln Ile Pro Ala Ser Thr		
	235	240	245
	Pro Gln Asn Pro Ala Thr Ser Gln His Pro Pro Pro Pro Gly His		
30	250	255	260
	Arg Ser Gln Ala Pro Ser His Arg Pro Pro Pro Pro Gly His Arg Val		
35	265	270	275 280
	Gln His Gln Pro Gln Lys Arg Pro Pro Ala Pro Ser Gly Thr Gln Val		
	285	290	295
	His Gln Gln Lys Gly Pro Pro Leu Pro Arg Pro Arg Val Gln Pro Lys		
40	300	305	310
	Pro Pro His Gly Ala Ala Glu Asn Ser Leu Ser Pro Ser Ser Asn		
	315	320	325

45 (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1050 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: cDNA

55

- (ix) FEATURE:
- (A) NAME/KEY: CDS
 - (B) LOCATION: 1..1041

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5      (ix) FEATURE:
          (A) NAME/KEY: mat_peptide
          (B) LOCATION: 85..1041

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(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 360..361

(D) OTHER INFORMATION: /note- "LFA-3/IgG fusion point"

ATG GTT GCT GGG AGC GAC GCG GGG CGG GCC CTG GGG GTC CTC AGC GTG 48
Met Val Ala Gly Ser Asp Ala Gly Arg Ala Leu Gly Val Leu Ser Val
-28 -25 -20 -15

30 ATA TAT GGT GTT GTG TAT GGG AAT GTA ACT TTC CAT GTA CCA AGC AAT 144
 Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn
 5 10 15 20

40 GAA CTG GAA AAT TCT GAA TTC AGA GCT TTC TCA TCT TTT AAA AAT AGG 240
Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg
40 45 50

GTT TAT TTA GAC ACT GTG TCA GGT AGC CTC ACT ATC TAC AAC TTA ACA 288
Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr
55 60 65

45 TCA TCA GAT GAA GAT GAG TAT GAA ATG GAA TCG CCA AAT ATT ACT GAT 336
Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp
70 75 80

50 ACC ATG AAG TTC TTT CTT TAT GTC GAC AAA ACT CAC ACA TGC CCA CCG 384
Thr Met Lys Phe Phe Leu Tyr Val Asp Lys Thr His Thr Cys Pro Pro
85 90 95 100

55 TGC CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC 432
Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
105 110 115

CCA AAA CCC AAG GAC ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA 480
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr

	120	125	130	
5	TGC GTG GTG GTG GAC GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn 135 140 145			528
10	TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg 150 155 160			576
	GAG GAG CAG TAC AAC AGC ACG TAC CGG GTG GTC AGC GTC CTC ACC GTC Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val 165 170 175 180			624
15	CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG GTC TCC Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser 185 190 195			672
20	AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys 200 205 210			720
25	GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp 215 220 225			768
30	GAG CTG ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe 230 235 240			816
	TAT CCC AGC GAC ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu 245 250 255 260			864
35	AAC AAC TAC AAG ACC ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe 265 270 275			912
40	TTC CTC TAC AGC AAG CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly 280 285 290			960
45	AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr 295 300 305			1008
50	ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA TGAGTGC GG Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys 310 315			1050

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 347 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5	Met	Val	Ala	Gly	Ser	Asp	Ala	Gly	Arg	Ala	Leu	Gly	Val	Leu	Ser	Val	-28	-25	-20	-15
	Val	Cys	Leu	Leu	His	Cys	Phe	Gly	Phe	Ile	Ser	Cys	Phe	Ser	Gln	Gln	-10	-5	1	
10	Ile	Tyr	Gly	Val	Val	Tyr	Gly	Asn	Val	Thr	Phe	His	Val	Pro	Ser	Asn	5	10	15	20
	Val	Pro	Leu	Lys	Glu	Val	Leu	Trp	Lys	Lys	Gln	Lys	Asp	Lys	Val	Ala	25	30	35	
15	Glu	Leu	Glu	Asn	Ser	Glu	Phe	Arg	Ala	Phe	Ser	Ser	Phe	Lys	Asn	Arg	40	45	50	
	Val	Tyr	Leu	Asp	Thr	Val	Ser	Gly	Ser	Leu	Thr	Ile	Tyr	Asn	Leu	Thr	55	60	65	
20	Ser	Ser	Asp	Glu	Asp	Glu	Tyr	Glu	Met	Glu	Ser	Pro	Asn	Ile	Thr	Asp	70	75	80	
25	Thr	Met	Lys	Phe	Phe	Leu	Tyr	Val	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	85	90	95	100
	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	105	110	115	
30	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	120	125	130	
	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	135	140	145	
35	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	150	155	160	
40	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	165	170	175	180
	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	185	190	195	
45	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	200	205	210	
	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	215	220	225	
50	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	230	235	240	
55	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	245	250	255	260
	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	265	270	275	

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
280 285 290

5 Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
295 300 305

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
310 315

[illegible]